Introduction

# Exploring phonological diversity through principal component analysis

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## Introduction

- Areal typology is undergoing a revolution as computational methods are being applied to new 'big data' regional datasets (e.g. O'Connor and Muysken, 2014; Reesink et al., 2009; Wichmann and Good, 2014)
- Major goals:
  - Identify typological structure in large regional datasets
  - Identify areal vs. genetic patterns in such datasets (clarify role of language contact in regional typology)

# A tool for areal typology: PCA (correlation and clustering)

- One promising tool to identify large-scale typological patterns is **principal component analysis** (PCA)
- PCA reorganizes a set of correlated variables into new subsets of linearly uncorrelated variables (the 'principal components')
- The principal components (PCs) 'absorb' the correlations in the original variables
  - Examining the PCs informs one about correlations in the data

## A tool for areal typology: PCA (dimension reduction)

- PCs are also **ranked** in terms of what percent of the variance in the dataset each PC accounts for
- In datasets where the original variables exhibit significant correlation:
  - the 'early' PCs (PC1, PC2, ...) account for much of the variance
  - while the later PCs account for little of the variance
- Later PCs can be discarded for many purposes, making PCA a tool for exploratory dimension reduction for high-dimension datasets
- Since early PCs account for the major variance in the dataset, they identify major dimensions of **typological differentiation** in a dataset

# PCA and phonological areal typology in South America

- We demonstrate the utility of PCA by applying it to a dataset of South American phonological inventories (SAPhon), to answer the following questions:
  - How is the phonological diversity of South America structured?
    - What are the major typological parameters of differentiation?
  - What areal patterns are detectable?
  - What genetic patterns do we find?

#### Preview of results

- We present evidence for a strong areal signal in the Andean and Circum-Andean region and its subregions, separating it from Amazonia
- We will also show evidence for a smaller linguistic area in Northwest Amazonia
- We will argue that languages in South America differ as to whether the locus of phonological contrast is in their consonant system or vowel system
- We will demonstrate that contrasts in nasality and length on vowels are both significant dimensions of differentiation for inventories in South America

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## The data: SAPhon

- Our analysis of areality and typological patterning in South American phonologies is based on the SAPhon dataset
- SAPhon (South American Phonological Inventory Database) is an online database of phonological inventories of languages of South America (Michael et al., 2016)
  - http://linguistics.berkeley.edu/~saphon/en/
- SAPhon houses phonological inventories for 363 languages
  - All languages for which published inventories are available (plus many for which they aren't):  ${\sim}90\%$  of living South American languages
  - 104 more than the number of languages with ISO codes in South America (due to inclusion of extinct languages, and some finer-grained classification)

#### Modeling the SAPhon dataset using a vector space

- To apply PCA it is necessary to model the SAPhon inventories as points in a (301-dimensional) vector space:

  - For a given segment vector (e.g., p), a language exhibits a magnitude of 1 if it has this segment in its inventory, and 0 if it doesn't
  - The combination of these 1 and 0 values for the segment vectors positions each of the 363 SAPhon languages in the vector space

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# Understanding PCA

- PCA is a transformation (a rotation) of the original set of basis vectors into a new set of basis vectors (= the 'principal components')
  - This rotation eliminates correlations between the basis vectors in the dataset
  - These new vectors are oriented in the 'directions' of greatest variance in the dataset

• As with all rotations in a vector space, the new basis vectors are defined in terms of linear combinations of the old basis vectors

Conclusion Refere

# Understanding PCA

• Dataset with original set of variables (vectors)



Conclusion Reference

# Understanding PCA

- Dataset with original set of variables (vectors) and new PCs
- PC1 oriented in direction of greatest variance in the dataset



# Understanding PCA

• The PCs are a linear combination of the original basis vectors:  $P\vec{C}1 = sin(\alpha)\vec{v1} + cos(\alpha)\vec{v2} = \frac{1}{\sqrt{2}}\vec{v1} + \frac{1}{\sqrt{2}}\vec{v2}$ (1)(2)  $P\vec{C}2 = sin(\beta)\vec{v1} + cos(\beta)\vec{v2} = \frac{1}{\sqrt{2}}\vec{v1} - \frac{1}{\sqrt{2}}\vec{v2}$ PC1 PC2 v1/√2 v1/√2 ß α  $\alpha = 45^{\circ}$  $\beta = 135^{\circ}$ v2/√2 √2/√2 E > < E > э.

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# SAPhon PCs

- The PCs obtained by carrying out PCA on the original SAPhon basis vectors are thus linear combinations of the segment vectors
- The linear sum specifies the positive and negative weights accorded each segment in calculating the given PC:
  - e.g. PC1 = 0.140I + 0.137ts + 0.128J + 0.114k + 0.122a: ... - 0.359 $\tilde{i}$  - 0.348 $\tilde{a}$  - 0.315 $\tilde{e}$  - 0.312 $\tilde{u}$  - 0.306 $\tilde{o}$
- Each PC resembles a pair of weighted phonological inventories:
  - A **positive inventory** that characterizes the positive extremum of that PC
  - A **negative inventory** that characterizes the negative extremum of that PC

#### Variance explained by PCs

- A comparatively small number of the 301 PCs are responsible for explaining the majority of the variance in the dataset
- PC1 = 14.2%, PC2 = 7.6%,  $PC3 \approx 5.4\%$ , ...



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## Variance explained by PCs

- A comparatively small number of the 301 PCs are responsible for explaining the majority of the variance in the dataset
- PC1 = 14.2%, PC2 = 7.6%,  $PC3 \approx 5.4\%$ , ...
- Due to the rapid decrease in variance explained by the successive PCs, we can focus on the largest PCs to identify the significant 'typological structure' of the SAPhon phonological inventories
- For each of the first 5 PCs, we can examine both areal and genetic patterns that are revealed

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# PC1: positive coefficients

- PC1 explains 14.2% of the variance in the data
- The segments with the largest positive coefficients include affricates, palatals, and laterals



# PC1: negative coefficients

- Negative coefficients are slightly larger than positive coefficients
- The segments with the largest negative coefficients include nasal vowels, i, and mid vowels



#### PC1: areal signal

• PC1 yields a strong positive signal in the Andean and Circum-Andean region



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Conclusion Reference

# PC1: genetic signal

 PC1 shows a negative genetic signal including the Tucanoan (p<1.0E-13), Tupí (p<1.0E-11), and Macro-Ge (p<1.0E-4) families (using Kolmogorov-Smirnov Test)



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Conclusion Reference

## PC1: genetic signal

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#### PC1: summary

- Positive segments: alveolar and palatal laterals, affricates, fricatives, and nasals
- Negative segments: nasal vowels, i
- Positive component yields a strong areal signal in the Andes and Circum-Andean area, including Patagonia
  - Independently identifies this phonological area, first found using a Naive Bayesian Classifier method (Michael et al., 2014)

• Negative component shows a genetic signal from Tucanoan, Macro-Ge, and Tupí families

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# PC2: positive coefficients

- PC2 explains 7.6% of the variance in the data
- The segments with the largest positive coefficients include the voiced stops



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# PC2: negative coefficients

- Negative coefficients are larger than positive coefficients
- All of the segments with the largest negative coefficients are long vowels



#### PC2: areal signal

• PC2 does not display a strong areal signal distinct from genetic relationships



#### PC2: genetic signal

 PC2 shows negative genetic signal from Arawak (p<1.0E-5) and Yanomam (p<1.0E-4)</li>



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# PC2: genetic signal

 PC2 shows negative genetic signal from Arawak (p<1.0E-5) and Yanomam (p<1.0E-4)</li>



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#### PC2: summary

- Positive segments: voiced stops
- Negative segments: long vowels
- Negative component shows a strong genetic signal associated with Yanomam, and other families also cluster together
- We see a large negative dispersion with the most strongly negative languages displaying vowel length contrasts for many vowels

# PC3: positive coefficients

- PC3 explains 5.4% of the variance in the data
- The segments with the largest positive coefficients include the voiced stops, tone, and aspirated stops
- Positive coefficients are much larger than negative coefficients



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## PC3: negative coefficients

• The segments with the largest negative coefficients include the nasal stops and approximants



#### PC3: areal signal

• PC3 shows a strong positive signal in Northwest Amazonia



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#### PC3: genetic signal

 PC3 shows a strong negative genetic signal associated with Tupí (p<1.0E-5)</li>



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#### PC3: genetic signal

 PC3 shows a strong negative genetic signal associated with Tupí (p<1.0E-5)</li>



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#### PC3: summary

- Positive segments: voiced stops, tone
- Negative segments: nasal stops, approximants
- Positive component yields a strong areal signal in Northwest Amazonia
  - Identifies this well known linguistic area (see, e.g. Aikhenvald, 2002) on the basis of phonological inventories alone
- This positive signal reflects languages that have processes of nasal harmony rather than underlying nasal stops
- Negative component shows a genetic signal from Tupí

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# PC4: positive coefficients

- PC4 explains 4.6% of the variance in the data
- The segments with the largest positive coefficients include  $\beta$ , i, palatals, and mid vowels



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# PC4: negative coefficients

- Negative coefficients are larger than positive coefficients
- The segments with the largest negative coefficients are ejectives, aspirated stops, laterals, and uvulars



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#### PC4: areal signal

• PC4 shows a strong negative signal in the Southern Andean and Circum-Andean region, including Patagonia



#### PC4: genetic signal

 PC4 shows a positive genetic signal associated with Tupí (p<1.0E-5) and Panoan (p<1.0E-4)</li>



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### PC4: genetic signal

 PC4 shows a positive genetic signal associated with Tupí (p<1.0E-5) and Panoan (p<1.0E-4)</li>



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# PC4: summary

- Positive segments:  $\beta$ , i, palatals
- Negative segments: ejectives, aspirated stops, laterals, uvulars
- Negative component shows further support for a strong areal signal in Southern Andean and Circum-Andean region
  - Identifies this important sub-area of the Andean and Circum-Andean area also found by Michael et al. (2014)
- Positive component shows a genetic signal from Tupí and Panoan

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## PC5: positive coefficients

- PC5 explains 3.9% of the variance in the data
- The segments with the largest positive coefficients are mid vowels, w, and glottals



# PC5: negative coefficients

- Negative coefficients are slightly larger than positive coefficients
- The segments with the largest negative cofficients are palatals, affricates, and i



## PC5: areal signal

• PC5 shows a negative signal in the Central-Northern Andean region and a positive signal in the east



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#### PC5: genetic signal

 PC5 shows a west/east divide illustrated by the Quechua (p<1.0E-9) and Carib (p<1.0E-4) families</li>



Conclusion Reference

#### PC5: genetic signal

 PC5 shows a west/east divide illustrated by the Quechua (p<1.0E-9) and Carib (p<1.0E-4) families</li>



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- Positive segments: mid vowels
- Negative segments: palatals, affricates, i
- There is a general divide, both genetic and areal, between a negative signal in the west and a positive signal in the east
  - The western negative region corresponds to the Central-Northern Andean and Circum-Andean sub-region identified by Michael et al. (2014)
- Overall, the signal is becoming weak by this point

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### Interim Summary: Areal results

- Examination of geographical distribution of extremal values of PCs 1–5 have identified known phonological areas in South America:
  - 1. Andean and Circum-Andean phonological area
    - 1.1 Southern Andean and Circum-Andean phonological sub-area
    - 1.2 Central-Northern Andean and Circum-Andean phonological sub-area
  - 2. Northwest Amazonian phonological area
- Whereas previous identification of these areas have relied on methods that require human insight and intuition (Naive Bayes Classifier approaches; Michael et al. (2014)), in the PCA approach can these results emerge more directly from the data

# Identifying phonological 'types'

- Since the PCs identify the major dimensions of phonological variation in South America, we can develop a 'continental typology' of phonological inventories
- Major phonological types can be identified by examining how inventories cluster with respect to PC1 and PC2
  - Hierarchical clustering using a Euclidean distance measure and Ward's clustering criterion
- Sampling languages in each cluster allows us to identify their major features

# Phonological types in South America

- What major types can we extrapolate from PCA?
- What are the clusters and what are their general profiles?



# Quadrant 1: +PC1, +PC2

- Features: large consonant inventories (laterals, affricates, voiced stops) and small vowel inventories
- Example language: Salasaca Quechua (Quechua)

Consonants	Bilabial	Alveolar	Post- alveolar	Palatal	Velar	
Aspirated stop	$\mathbf{p}^{\mathbf{h}}$	t <sup>h</sup>			k <sup>h</sup>	
Plain/voiced stop	рb	t d			k g	
Affricate		ts	t∫			Vowels
Fricative		s z	∫3		x	High
Nasal	m	n		л		Low
Approximant				j	w	
Tap, flap		ſ				
Lateral		1				

owels	Front	Central	Back
ligh	i		u
ow		a	

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## Quadrant 2: +PC1, -PC2

- Features: large consonant inventories (laterals, affricates), moderate vowel inventories (long vowels)
- Example language: Chamicuro (Arawak)

Consonants	Bilabial	Alveolar	Post- alveolar	Retroflex	Palatal	Velar	Glottal				
Stop	р	t				k	?				
Affricate		ts	t∫	tş				Vowels	Front	Central	Back
Fricative		S	ſ	ş			h	High	i i:		u u:
Nasal	m	n			л			Mid	e e:		o o:
Approximant					j	w		Low		a a:	
Tap, flap		ſ									
Lateral		1			Y						

# Quadrant 3: -PC1, -PC2

- Features: small consonant inventories, large vowel inventories (nasal and long vowels)
- Example language: Karitiâna (Tupí)

Consonants	Bilabial	Alveolar	Palatal	Velar	Glottal
Stop	р	t		k	
Fricative		S			h
Nasal	m	n	л	ŋ	
Approximant				w	
Tap, flap		ſ			

Vowels	Front	Central	Back
High	i ĩ i: ĩ:	i î i: î:	
Mid	e ẽ e: ẽ:		o õ o: õ:
Low		a ã a: ã:	

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## Quadrant 4: -PC1, +PC2

- Features: moderate consonant inventories (voiced stops), moderate vowel inventories (nasal vowels)
- Example language: Siona (Tucanoan)

Consonants	Bilabial	Alveolar	Post- alveolar	Palatal	Velar	Labio- velar	Glottal
Stop/affricate	p b	t d	t∫		k g	k <sup>w</sup> g <sup>w</sup>	?
Fricative		s z				h <sup>w</sup>	h
Nasal	m	n					
Approximant				j		w	

Vowels	Front	Central	Back
High	i ĩ	iĩ	u ũ
Mid	e ẽ		οõ
Low		a ã	

# Conclusion

- In South America, whether languages make a large number of contrasts in their vowels is very significant in 'typing' languages
  - Nasal vs. oral is one of the most significant dimensions of variation
  - Length contrasts are also an important parameter of differentiation
- PCA is successful in producing this continental typology as well as in identifying important linguistic areas such as the Andean and Circum-Andean region and Northwest Amazonia
- This work provides a starting point for more quantitatively rigorous analyses of areality

Introduction

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Conclusion References

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